

11. The method of claim **1**, wherein the molecular target comprises a tag moiety, and the aptamer is a high affinity binding partner to at least a portion of the tag moiety of the molecular target.

12. The method of claim **11**, wherein the tag moiety is selected from a fluorescent protein or fragment thereof, a poly-His tag, a maltose binding protein tag, an albumin-binding protein tag, a calmodulin binding peptide tag, a glutathione S-transferase tag, a chitin binding protein tag, FLAG-tag, HA-tag, Protein A tag, and combinations thereof.

13. The method of claim **1**, wherein the aptamer is selected from a non-naturally occurring aptamer and a naturally occurring aptamer.

14. The method of claim **1**, wherein the aptamer is selected from a peptide aptamer, a DNA aptamer, and an RNA aptamer.

15. The method of claim **1**, wherein said aptamer is an RNA aptamer comprising:

a core region comprising a nucleotide sequence of any one of SEQ ID NOs:1-13.

16. The method of claim **1**, wherein the aptamer binds to a portion of a fluorescent protein selected from GFP, eGFP, CFP, eCFP, YFP, and eYFP.

17. The method of claim **1**, wherein the aptamer is immobilized on a solid support.

18. The method of claim **1**, wherein said molecular target comprises two or more associated biomolecules, and said analyzing comprises:

identifying each of the two or more associated biomolecules of the molecular target.

19. The method of claim **18**, wherein said identifying comprises:

subjecting the molecular target to mass spectrometry to detect each of the two or more associated biomolecules of the molecular target.

20. The method of claim **1**, wherein said analyzing comprises:

subjecting the molecular target to mass spectrometry to detect one or more posttranslational modifications of said molecular target.

21. The method of claim **20**, wherein the one or more posttranslational modifications is selected from methylation, acetylation, phosphorylation, sumoylation, or combinations thereof.

22. The method of claim **1**, wherein said molecular target comprises nucleotide oligomers and said analyzing comprises:

isolating the nucleotide oligomers from the molecular target and

subjecting said isolated nucleotide oligomers to an amplification reaction, a sequencing reaction, or a combination thereof to identify the isolated nucleotide oligomers of the molecular target.

23. The method of claim **1**, wherein said analyzing comprises:

subjecting the molecular target to cryo-electron microscopy to determine the three-dimensional structure of the molecular target.

24. The method of claim **23**, wherein said molecular target comprises two or more associated biomolecules, and said subjecting is carried out to determine the three-dimensional structure of the two or more associated biomolecules of the molecular target.

25. The method of claim **1**, wherein the sample is a cell or tissue lysate, a plasma sample, a serum sample, a blood sample, an exosome sample, or other biological sample.

* * * * *